



REMARKS

Entry of the foregoing and favorable reconsideration and reexamination of the subject matter pursuant to and consistent with 37 C.F.R. § 1.112 is respectfully requested.

Applicant requests consideration of these additional remarks which supplement the response file on June 29, 1999. It will be demonstrated below that the current claims of record are clearly novel and unobvious over the cited prior art of record and should be taken into consideration by the Examiner.

It should be recalled that the present claims of record are directed to a method aiming at inhibiting the replication of an immunodeficiency retrovirus wherein 100% inhibition of the retrovirus in primary cultures of monocytes in the host is achieved using selected muramyl peptides.

It should be brought to the immediate attention of the Examiner that:

- (1) the claims of record encompass 100% inhibition of the retrovirus which is not disclosed in the prior art; and
- (2) this inhibition was demonstrated in primary cultures (cultures prepared directly from the tissues of an organism) of monocytes of the host, which is also not demonstrated in the cited prior art.

Applicant submits that the demonstration in the present invention of 100% inhibition of a retrovirus in primary cultures of monocytes is an extremely important aspect of the present invention that must be taken into

consideration by the Examiner in analyzing the prior art. This is because it is known in the art that the use of primary cultures of monocytes is a more scientifically sound *in vitro* system for testing drugs or medicaments for the inhibition of HIV-1 than in those cell lines disclosed in the prior art, as will be discussed more extensively below under the heading HIV-1 replication.

It should be emphasized, as will be discussed in greater detail below, that the cited prior art teaches the use of muramyl peptides for inhibiting HIV-1 infection using strains that are infected by T-Tropic HIV-1 strains. The prior art is silent with respect to the use of muramyl peptides for inhibiting immunodeficiency retroviruses in the presently claimed primary cultures of monocytes which are infected by M-Tropic HIV-1 strains.

HIV-1 REPLICATION

It is now known that HIV-1 needs to replicate in macrophages or dendritic cells prior to spreading to T lymphocytes. At the early stages of HIV-1 infection, shortly after seroconversion and during the asymptomatic period of AIDS, macrophage tropic or M-Tropic strains of the virus predominate.

In contrast, in the late stages of HIV-1 disease in association with CD4 T cell decline and progression to AIDS, T cell lines or T-Tropic strains of HIV-1 predominate.

The mechanism behind entry of HIV-1 gp120 at the different stages of HIV-1 disease is different. It is now known that besides binding to the CD4 receptor, interaction of the V3 loop in gp120 with a second receptor or co-receptor is required for gp120 to enter the cells. At the early stages of HIV-1 disease the co-receptor required for the gp120 to enter the macrophages

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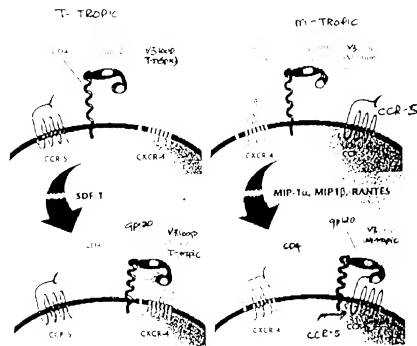
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was discovered to be the CCR-5 co-receptor. In contrast, in the late stages of the disease, the co-receptor required to enter the cells was discovered to be fusin or the CXCR-4 co-receptor. These receptors are different as can be seen schematically below



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Both of the co-receptors were discovered to be chemokine receptors that belong to the family of G-coupled protein receptors, which have seven transmembrane regions. The fact that these receptors have seven transmembrane regions is important, since resistance to HIV-1 infection, including T cell depletion, was discovered in certain individuals bearing a mutant allele of the CCR-5 chemokine co-receptor.

This mutant CCR-5 co-receptor lacks the three transmembrane segments of the wild CCR-5 receptor and was unable to support membrane fusion by both the primary and dual-tropic virus env. Hence, it was concluded that homozygous individuals having this mutant CCR-5 receptor are highly resistant to HIV-1 infection.

The above supports the theory that the CCR-5 receptor plays a primary role in the replication of HIV-1 which replication then leads in the later stages of the disease to AIDS

Hence, it is more scientifically beneficial to find drugs that target the early stages of HIV-1 infection using the M-Tropic HIV-1 strain at an early stage of infection, thus either diminishing or preventing the total onset of AIDS. This even the more so since macrophages serve as a reservoir for the virus and this reservoir is less sensitive to antiretroviral effects than T-lymphocytes.

Therefore, in the present invention inhibition of the replication of HIV-1, in the presently claimed process was demonstrated in **primary cultures of monocytes** (monocytes are precursors to macrophages) which cultures are the scientific tools of choice to use in drug evaluation experiments for HIV-1 inhibition, as explained above.

In contrast the **use of cell lines** to test for drugs which inhibit HIV-1 is highly artificial and drugs that can inhibit T-Tropic HIV replication are not necessarily effective against replication of M-Tropic viruses in macrophages. This has been demonstrated by the fact that SDF-1 (Stromal cell derived factor), the ligand for CXCR-4, can inhibit virus entry into cell lines, but has absolutely no effect of preventing M-Tropic HIV-1 entry and infection in macrophages or primary T-lymphocytes.

Therefore, the fact that the Applicant has demonstrated 100% inhibition of a retrovirus in primary cultures of monocytes (M-Tropic HIV-1 strains) with the presently claimed muramyl peptides is an unexpected result which should distinguish clearly over the prior art of record where such a demonstration is not achieved. Rather the cited prior art teaches low inhibition of several muramyl peptides in cell lines which are T-Tropic strains of HIV-1.

These and other differences will be addressed in view of the issues brought to bear in the last Official Action.

35 U.S.C. §102(b)

The Examiner deems that Claims 14 to 21, 25, 26, 28 to 30 and 34 lack novelty in view of Schreck et al.

Furthermore, Claims 14 to 21, 25, 26, 28 to 30 and 34 lack novelty over Masihi et al.

Schreck et al.

Schreck et al. teach the use of muramyl peptides as **adjuvants** in potential vaccines against AIDS. By definition an adjuvant is an ingredient (as in a prescription or solution) that modifies the action of the principle ingredient. An adjuvant is not the active ingredient in a vaccine, as the skilled artisan well knows.

Furthermore, Schreck et al. disclose that it would be beneficial to select adjuvants that do not induce NF- κ B activation and particularly if the

vaccines are to be aimed at treating seropositive individuals, since it was believed that the **activation of NF- κ B purportedly enhanced HIV-1 expression.**

In fact, MDP (thr)-GDP was found **to be the only lipophilic, nonpyrogenic adjuvant that demonstrated lack of NF- κ B activation.** This teaching is apparent at page 188, 2nd column, lines 13 to 15 of Schreck et al.

Although two muramyl peptides, encompassed by the present claims were tested for NF- κ B activation, it was discovered that in the human Mono-Mac-6 cell line **NF- κ B activation was apparent using murabutide and murametide** as set forth in the sentence bridging column 1 and column 2 at page 190 of Schreck et al. Therefore, murametide and murabutide do not belong to the **selected** category of an adjuvant that could be foreseen for use with an AIDS vaccine.

Furthermore, it is apparent that there is no experimental evidence that the muramyl peptides utilized in Schreck et al., can inhibit the replication of immunodeficiency retroviruses. Thus, a skilled artisan can conclude nothing about whether the muramyl peptides in Schreck et al., have any inhibitory properties.

Therefore, Applicant submits that since Schreck et al., fails to teach the use of the claimed muramyl peptides as an active ingredient in a process to inhibit immunodeficiency retroviruses and, since the claimed muramyl peptides do not fall into the category of those being sought in Schreck et al., the presently claimed invention is not anticipated by Schreck et al.

Masihi et al.

Masihi et al. disclose that muramyl dipeptide can enhance monocyte/macrophage CSF in serum and promote nonspecific resistance against a variety of microbial pathogens including HIV infection of CD4⁺ H9 lymphocytes and U937 monocytic cells. However, this effect cannot be mediated by macrophage-CSF which itself has been shown to increase viral replication (see, Annex I, page 33, last paragraph, left column)

The Examiner refers to page 397 of Masihi et al. where murabutide was taught to be used as an **adjuvant** in human clinical trials. As discussed above, an adjuvant is solely used as a vehicle to modify the action of the active ingredient. Masihi et al. fails to teach that murabutide can be used in a process to treat immunodeficiency retroviruses directly.

Indeed, the cell lines used in the experiments in as the active ingredient in the manufacture of a medicament are H9, KE37/1 and U937 which are only infectable by T-Tropic HIV-1 strains. In contrast the present invention uses primary cultures of monocytes which are only infectable by M-Tropic HIV-1 strain. Thus, Masihi et al. disclose muramyl peptides for targeting the late stages of HIV-1, while the muramyl peptides in the process of the presently claimed invention target the early stage of HIV-1.

Therefore, in view of the above, Applicant submits that the presently claimed invention is not anticipated by Masihi et al.

35 U.S.C. §103(a)**Masihi et al.**

Masihi et al. fail to teach the skilled artisan that murabutide can be used in a medicament as the active ingredient for inhibiting the replication of a retrovirus. Rather Masihi et al. teach the use of murabutide only as an adjuvant.

Furthermore, a skilled artisan would not extrapolate the results of a muramyl dipeptide disclosed in Masihi et al. to include all muramyl peptides, since as taught in Masihi et al. at page 189 under Reagents, different muramyl peptides have different properties.

Only if the Examiner deems that a skilled artisan would indeed extrapolate results from MDP to the rest of the muramyl peptides, Applicant would like to point out that Masihi et al. discloses only 67% reduction of the p24 antigen using MDP and only a 38% inhibition on day 14 using infected CD4⁺ KE37/L lymphocytes and further teaches that 1000 µg/ml dosages were more effective.

Moreover, Figure 3 clearly demonstrates that less than 50% inhibition of p24 antigen using MDP at 1,000 µg/ml is achieved in U937 monocytic cells. **This percentage inhibition cannot be compared to the 100% inhibition achieved by the claimed muramyl compounds of the present invention,** which Applicant submits is an unexpected result.

Furthermore, Masihi et al. teach using 1000 µg/ml MDP which is an extremely high dosage and the side effects of MDP, including pyrogenicity and inflammatory reactions would be enormous at this particular dosage. This would discourage the skilled artisan to pursue a medicament using MDP.

Finally, in Masihi et al., the cell lines in which the muramyl peptides were tested for inhibition of HIV-1 are T-Tropic HIV-1 strains. Masihi et al. is silent with respect to the testing of these compounds in M-Tropic HIV-1 strains which clearly distinguishes the presently claimed invention from this reference, as discussed above.

In other words, Masihi et al. teach that MDP can inhibit HIV-1 infection in the late stages of the disease. Masihi et al. does not disclose nor demonstrate that MDP or any other muramyl peptide for that matter can target the early stages of HIV-1 infection, which is the most important stage to target.

It should be clear that silence in a reference is not a proper basis to maintain an obviousness rejection.

From the foregoing, favorable action in the form of a Notice of Allowance is respectfully requested and earnestly solicited.

If the Examiner has any questions concerning this application, he is requested to contact the undersigned at (703) 205-8000 in the Washington, D.C. area.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account No. 02-2448 for any additional fees

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required under 37 C.F.R. § 1.16 or under 37 C.F.R. § 1.17;
particularly, extension of time fees.

Respectfully submitted,

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Host factors in the pathogenesis of HIV disease

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Summary: Host factors play an important role in determining rates of disease progression in human immunodeficiency virus (HIV)-infected individuals who are able to suppress the host immune system by infecting CD4⁺ T cells. The normal, protective, immune responses and the subsequent development of proinflammatory cytokines that develop as a result of this immune response are important. The recognition that certain chemokine receptors serve as necessary co-receptors for HIV entry into target cells as well as the fact that ligands for these receptors can modulate the efficiency of HIV infection has expanded the number and scope of host factors that may impact the pathogenesis of HIV disease. This area of investigation will no doubt yield novel therapeutic strategies for the treatment of HIV disease, however, caution is warranted in light of the enormous complexity of the pathogenic system and the wide interplay and the uncertainty inherent in manipulating these systems.

HIV-infected long-term seropositive individuals represent an excellent model to study potential host factors that may impact HIV disease pathogenesis. Genetic factors certainly have a major impact, since immune responses mounted by the host in the region of a polymorphism in the gene for the HIV co-receptor CC chemokine receptor 5 (CCR5), which serves as a co-receptor for macrophage (M)-tropic viruses at HIV infection, affect the degree of protection against HIV infection in individuals homozygous for the polymorphism and some degree of protection against disease progression in HIV-infected heterozygotes. HIV species, including the recently isolated CRF01_AE, CRF02_AG, CRF07_BC, and CRF08_BC, and the associated antibody responses and their impact on disease progression are promising areas for future investigation.

Introduction

The pathogenesis of human immunodeficiency virus (HIV) disease is complex and influenced by both viral and host factors (1). The multifactorial nature of HIV disease pathogenesis is reflected in the highly variable rates of disease progression that are observed in individuals infected with HIV. The importance of host factors in modulating rates of disease progression is further underscored by the observation that seropositive individuals who were apparently infected from a single source, but who later experienced widely variable rates of disease progression, have been shown to have different levels of expression of polymorphisms in the CCR5 gene (2). The recent discovery that the CCR5 gene is located on chromosome 3 and has been quite recently shown to be involved in the regulation of the immune system during certain autoimmune diseases (3,4) has further

in have confirmed earlier work that demonstrated high levels of viral replication throughout the course of HIV infection (7-9) and have greatly expanded our understanding of the dynamics of HIV replication in vivo. The remarkable consistency in quantitative estimates of the rate of turnover of plasma virus particles supports a discussion regarding the observed variations in rates of disease progression. In this regard, future studies will need to assess whether the rate of viral turnover varies according to stage of disease or whether it is an intrinsic characteristic of HIV infection. In either case, it is necessary to involve host factors in order to explain the great variability in rates of clinical disease progression.

A delicate balance among a wide array of host factors likely determines the rate of viral replication in HIV-infected individuals. Subversion of the human immune system by HIV (i.e. infection of cells that are critical components of an intact immune system; induction of the secretion of proinflammatory cytokines; and utilization of these products of immune activation for the permissive advantage of the virus) usually tips the balance in favor of the virus. The recent discovery that certain chemokine receptors (for example, CC chemokine receptor (CCR5), CXCR chemokine receptor (CXCR4), CCR3 (CCR1b), STRLW3, Bimx, and BDB) are utilized by different strains of HIV as co-receptors to gain entry into cells has greatly expanded the number of candidate host factors that may influence the pathogenesis of HIV disease (10-18). The ability of the chemokine ligands of these receptors to block HIV entry into target cells and thereby tip the balance of immune control over virus replication in favor of the host is a new concept in the field of HIV pathogenesis that has major implications for potential therapeutic intervention.

Genetic factors may determine the outcome of interactions between virus and host in several ways. First, the host's HIV-specific immune responses are constrained by the individual's major histocompatibility complex (MHC) alleles. In addition, the recently discovered genetic defect in the CCR5 gene has a major impact on susceptibility to HIV infection in individuals homozygous for the defect, and on disease progression in HIV-infected individuals heterozygous for the defect. HIV-specific cellular and humoral immune responses likely play an important role in the control of viral replication; although previous estimates of protective immunity have not been exhaustive, however, recent studies have shown that qualitative as well as quantitative features of these immune responses may be important in modulation of disease progression.

Expanding on these recent observations, future investigations of HIV infection should lead to the design of novel therapeutic strategies. The goal is to tip the balance in favor of the host.

One over-vital implication may appear to be simple. However, the extraordinary complexity of manipulating host factors to prevent or delay the onset of clinical complications. This latter point is highlighted by the negative outcomes of human trials for antiviral agents that targeted molecules thought to be directly involved in the pathogenesis of virus (i.e. example: lipopeptides, nucleoside analogs, HIV protease inhibitors, for "NRTI" class). The need to consider interplay between the context of a balanced pre- and anti-inflammatory mediators and the need to consider direct interactions (e.g. anti-p24, pleiotropic cytokine network apply not only to virus (20) but to HIV disease as well.

Cytokines and HIV disease: dysregulation of cytokine production

A highly complex network of cytokines operates to regulate the immune system. This network is redundant and pleiotropic, and operates in an intricate and paracrine manner to stimulate or suppress cellular proliferation and differentiation, and to modulate immune function (21). Chronic immune activation induced by HIV infection and associated opportunistic infections results in dysregulation of the cytokine network. Many of the observed alterations in cytokine production contribute to HIV pathogenesis by further simplifying viral replication, suppressing the ability of the immune system to mount a strong antiviral response, and inducing cytokine-mediated sympathic effects (1, 22-24).

Similar to other chronic infections, HIV infection is associated with increased expression of proinflammatory cytokines, especially during the later stages of disease (25). High levels of TNF- α , IL-1 β , and IL-6 are secreted by peripheral blood mononuclear cells (PBMC) (25-30) and macrophages (31-34) from HIV-infected subjects. TNF- α (25-28) and IL-6 are also found at elevated levels in the serum (35-37), cerebrospinal fluid (38-40), and tissues (34, 41). High levels of expression of these cytokines is well established in HLN (10, 12, 50, 42, 43, 44, 45). IL-6 are particularly elevated in lymphoid tissue. In the case of HIV, replication can affect the course of IL-6 as (46, 47, 48). Chronically activated macrophages (C8, T cell, 49, 50) and macrophages (51) are thought to be the most contributors to the elevated cytokine levels, whereas a dysregulated cytokine network is also observed in HIV.

In addition to alterations in cytokine production, the current state of the human HIV-specific immune system is characterized by a high level of immune activation. This is reflected by elevated levels of serum p24, increased turnover of CD4⁺ T cells, and increased levels of CD8⁺ T cells (52, 53). These observations are consistent with the concept of a chronic state of immune activation.

such as TNF and GM-CSF is attributed largely to their ability to enhance the secretion of activity of HIV-inducing proinflammatory cytokines [12, 13, 16, 19]. HIV production by infected T cells is stimulated by both the anti-inflammatory and the immunoprotective activity of such cytokines [10, 14, 15, 18, 20, 21, 22].

Although the role of proinflammatory and anti-inflammatory cytokines in the regulation of HIV replication has not been demonstrated conclusively, several lines of evidence suggest that these cytokines may be involved in regulating virus production. Administration of pentoxifylline, an inhibitor of the secretion and activity of TNF, to HIV-infected individuals was found to reduce HIV viremia in concert with a reduction in plasma levels of TNF- α [10, 101]. The role of proinflammatory cytokines in maintaining steady-state levels of HIV replication is suggested by the observation that *in vivo* infusion of a single bolus of IL-10 to HIV-infected subjects resulted in a rapid and modest albeit transient decrease in plasma viremia [10, Weissman & S. Fauce, unpublished data]. The kinetics of HIV suppression *in vivo* correlated with a dramatic reduction in the ability of cells from these subjects to be induced *in vitro* to secrete TNF- α and IL-1 β . Furthermore, IL-10 has been found to inhibit acute HIV infection in severe combined immunodeficiency (SCID) mice engrafted with human fetal thymus and liver [102]. The ability of IL-10 to suppress T-cell activation and proliferation likely also plays a prominent role in its ability to suppress HIV replication *in vivo* [103, 104].

In addition to the use of immunosuppressive cytokines which may depress HIV-inducing immune responses, cytokines which stimulate T cells or antigen-presenting cells have been administered to HIV-infected subjects for a number of years. The use of cytokine-based therapies aimed at immune reconstitution in HIV disease has expanded over the past several years, particularly with the development of potent antiretroviral therapies that limit the potential for cytokine-mediated increases in virus replication. In this regard, administration of IL-2 to asymptomatic HIV-infected subjects receiving zidovudine and zalcitabine therapy results in significant and sustained increases in CD4 $^{+}$ T cell numbers with no long-term effects on viremia [105, 106, 107]. Similar immune reconstitution therapies are being proposed for IL-2, IL-3, and IL-15 [108, 109, 110]. New studies are evaluating the use of IL-3-based therapies as potential immunotherapeutic agents. A particularly interesting cytokine-based immunotherapeutic approach is suggested by a recent report demonstrating that transfection of CD4 $^{+}$ T cells with GM-CSF encoding the HIV-1 gag gene and expression of a heterologous virus can protect T cells against HIV-1 infection [111]. This vector system

is based on the interference with viral co-receptor (p55 gp120) [112]. This effect may be due to the ability of GM-CSF to induce T cell activation [113, 114]. The combination of GM-CSF and IL-10 is a particularly effective approach that can synergistically enhance the expansion of CD4 $^{+}$ T cells. *In vitro* peripheral blood mononuclear

cells in addition to the known *in vivo* demonstrated previously, several studies indicate that HIV-1 infection is characterized by even greater HIV-induced immunosuppression than observed in these is the enzyme. Core co-receptor HIV suppressor factor(s). While T cell activity is an important component of CD8 $^{+}$ cell-mediated HIV suppression [115, 116], effector superlatants from cultures of activated CD8 $^{+}$ cells and T cells are able to inhibit HIV replication in CD4 $^{+}$ T cells and macrophages [117, 118]. CD8 antiviral factor (CAF) was described by Walker et al. [119, 120, 121]. CAF is a secreted factor that suppresses HIV replication in a non-MHC-restricted manner at the level of HIV RNA transcription [122-125] and acts on several known cytokines [126].

A distinct group of HIV suppressive factors secreted by CD8 $^{+}$ T cells was identified by Derube et al. [127]. These investigators attributed the HIV-suppressing activity of CD8 $^{+}$ cells to the combined activities of certain chemokine/chemokine receptors (i.e. chemokines), including macrophage inflammatory protein (MIP)-1 α , MIP-1 β , and RANTES (Regulated upon Activation, Normal T cell Expressed and Secreted). An unexplained finding in the study by Chakrabarti was that although the combination of the 3 chemokines MIP-1 α , MIP-1 β , and RANTES potentially suppressed the replication of several HIV strains, they had virtually no effect on the replication of the T-cell line adapted (TCLA) strain HIV-1 IND. Soon after this report, Frey et al. developed the very transmembrane orphan receptor fusin, previously known as XCR4 and HUM4R and currently designated CXCR4, as a coreceptor for T cell (T-tropic) strains of HIV-1 [128]. In addition, three groups described a novel chemokine receptor of CD8 $^{+}$ which bound MIP-1 α , MIP-1 β , and RANTES with a K_d of 128 [129]. Although these previous studies indicated a chemokine receptor that was a coreceptor for CD8 $^{+}$ macrophage as a coreceptor for HIV-1, the role of HIV-1 coreceptors from these different strains remains controversial. Thus, the discovery of chemokine receptors and their role in HIV-1 infection and progression has led to the discovery of HIV-1 coreceptors and their role in HIV-1 infection. The discovery of HIV-1 coreceptors has led to the discovery of HIV-1 coreceptors and their role in HIV-1 infection. The discovery of HIV-1 coreceptors has led to the discovery of HIV-1 coreceptors and their role in HIV-1 infection.

erated while the chemokine receptor CXCR4, an infection gate is blocked by the CXCR4 ligand stromal derived factor-1 (SDF-1). Many primary T-tropic HIV isolates exhibit a broad range of CCR usage, including CXCR4 and CCR5 (131, 132). The recent discoveries of other HIV co-receptors have already made obsolete the simplistic notion that CCR5 and CXCR4 are the only important co-receptors for M- and T-tropic strains of HIV respectively (1, 7, 18, 134).

Numerous cell types produce a variety of chemokines (135, 136), and modulation of the production of these factors may influence HIV replication in a strain-specific manner (1, 1). Therefore, the overall effect of immune activation and the selection of proinflammatory or immunoregulatory cytokines on HIV replication must now be considered in the context of potential influences on chemokine production, chemokine co-receptor expression, and the predominant viral quasispecies that is replicating *in vivo*. Chemokine production, induced during inflammation, is enhanced by several cytokines, including TNF- α , IL-1 β and immunoregulatory cytokines, such as IL-2 and IL-15 (135, 137-139). Thus, in HIV-infected subjects in the early stages of disease, the ability of TNF- α to stimulate β -chemokine production and thereby suppress M-tropic entry may override its HIV-inducing effects; however, in individuals harboring predominantly T-tropic quasispecies in the later stages of HIV disease, only the HIV-inducing activity of TNF- α would be influential. In fact, TNF- α -mediated induction of β -chemokine secretion may actually enhance entry and replication of T-tropic strains of HIV (A. Kinter & A.S. Fauci, unpublished data) (Fig 2).

Similarly, cytokines that modulate the expression of chemokine receptors would be expected to exert variable strain-dependent effects on HIV replication and spread. In this regard, IL-7 has been shown to upregulate the expression of the

T-tropic co-receptor CCR5 (140, 141). The puzzling bottleneck in HIV transmission that so heavily favors emergence of M-tropic, non-syncytium-inducing (NSI) strains of virus in the new host (142, 143) may in part be due to the differential regulatory patterns of the relevant HIV co-receptors (140, 143). In this regard, CCR5 expression is predominantly seen in pre-activated, mature T cells (i.e. CD45^{hi}CD45RA^{hi}CD45RO^{hi}), whereas CXCR4 expression is seen in naive, immature T cells (i.e. CD45^{lo}CD45RA^{hi}CD45RO^{lo}). It is therefore plausible that the profound degree of immune activation that occurs during acute HIV infection may result in high expression of CCR5 and low expression of CXCR4. M-tropic and X-tropic pathogens may differentially modulate expression of HIV co-receptors and thereby exert selective pres-

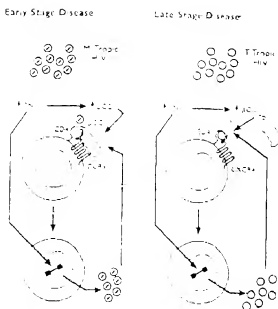


Fig. 2. Proinflammatory cytokines, such as TNF- α , have potentially dichotomous effects on HIV replication. During early stages of HIV disease, entry of M-tropic strains of the virus is predominant. Although TNF- α can transiently upregulate HIV expression in infected cells, it also simultaneously induces expression of the β -chemokine receptors CCR5, CXCR4, and MCP-2. These chemokines are specific for M-tropic HIV strains. Blockade of entry of HIV into target cells by chemokines. T-tropic strains of HIV may predominate in the late stages of HIV infection. In this situation, the induction of CXCR4 by TNF- α can up-regulate CXCR4, where via CXCR4 and not CXCR5 may enhance replication of T-tropic strains of HIV.

sure of HIV strains that are the more relevant in question. If appropriate, M. Merson, & A. S. Fauci, unpublished data).

The observation that the majority of cases of HIV infection in receptors that are utilized as HIV co-receptors act as potent inhibitors of viral entry has stimulated a renewed interest in the spectrum of HIV variability, especially with respect to the mechanisms whereby many strains of HIV infection, particularly those that are predominantly T-tropic, avoid or overcome the inhibitory effects of HIV co-receptors with respect to entry. The spectrum of HIV variability that is emerging in the context of HIV co-receptor utilization and its relationship to the spectrum of HIV variability is a topic that is currently being actively investigated. In this regard, it is important to note that the spectrum of HIV variability is not necessarily the same as the spectrum of HIV variability in the context of HIV co-receptor utilization. In this regard, it is important to note that the spectrum of HIV variability is not necessarily the same as the spectrum of HIV variability in the context of HIV co-receptor utilization.

PSMC from asymptomatic HIV-infected individuals harboring predominantly M-tropic HIV strains (143), but not in PSMC from individuals with more advanced disease harboring predominantly T-tropic HIV strains (146) (A. Kaiser & A.B. Fauci, unpublished data). Similarly, HIV isolates obtained longitudinally from infected individuals with rapid disease progression exhibit reduced sensitivity to inhibition by 3 chemokines *in vitro* (146-147).

A cautionary note about these potential therapies comes from the known association of the transition from M-tropic NSI to T-tropic/syncytium-inducing (SI) viruses with disease progression. The transition from an NSI to SI virus may occur by mutation of only a few amino acid residues predominantly in the envelope V3 loop (148-153). The HIV envelope V3 loop has also been shown to be a major determinant of co-receptor usage (156). Given the error rate of viral reverse transcription and the rapid dynamics of viral replication, mutations in the HIV envelope gene that encode SI strains must appear very early in disease, however failure of such mutants to emerge until late in the disease process indicates a change in the selective advantage of such a mutation during the course of disease progression. Because SI variants are able to use a broader range of entry co-receptors (for example, CXCR4) compared with NSI viruses, it is possible that SI variants emerge in response to high levels of β chemokines that block cellular entry of viruses which utilize CCR5 (i.e. predominantly NSI viruses) (152, 146-147). This potential effect of a chemokines should be investigated since the emergence of T-tropic HIV strains *in vivo* is associated with rapid CD4⁺ T cell decline and disease progression (157). Further caution is warranted in light of potential deleterious effects of the β chemokines on HIV replication in different cell types (119-138). The situation *in vivo* is no doubt highly complex, and multiple host factors as well as co-receptor expression in different tissue compartments likely determine the environment in which selection for NSI to SI variants is made (1, 140, 154).

While *in vitro* culture systems and cell line models have allowed investigators to identify numerous host factors that influence HIV replication and to delineate the mechanisms whereby these factors suppress or enhance viral replication, it is difficult to manipulate how manipulation of these factors will ultimately influence HIV replication *in vivo*. It is clear that host factors function within the context of an interactive immunoregulatory cytokine network and can have pleiotropic effects on HIV replication, some of which are viral strain-specific. Nevertheless, numerous host factors have proven to possess immunomodulatory potential that sound the bell for experimental and clinical research for the treatment of HIV disease.

Immune activation

Within months to 1 year following primary HIV infection, plasma viral titers appear to stabilize in a steady state or "set point" that is a strong prognostic indicator of the rate of disease progression (1). Characterizing this deceptively stable disease is a high rate of viral production and clearance (approximately 10¹⁰ copies of HIV RNA daily) (158-160), persistent, dysregulated CD4⁺ T-cell activation (161), and during clinically asymptomatic stages of HIV infection, persistent virus production serves as a potent source of immune activation and subsequent symptomatic disease. These activities in turn stimulate further viral replication.

Immune activation is essential for productive HIV infection of CD4⁺ T cells (161, 162), and agents that interfere with T-cell activation dramatically inhibit HIV replication in these cells (163-165). The role of immune activation in stimulating HIV replication *in vivo* is demonstrated by increases in viremia in HIV-infected individuals persistently or transiently exposed to exogenous immune stimuli. In this regard, HIV-infected natives of sub-Saharan Africa, who experience persistent immune activation due to chronic exposure to parasites and other pathogens harbor high viral loads associated with rapid progression of HIV disease (166, 168). Similarly, co-infection with opportunistic pathogens, such as active tuberculosis (167-170) or pneumocystis pneumonia (171), results in dramatic increases in levels of plasma HIV viremia that return to baseline upon successful treatment of the opportunistic infection (171). The source of elevated viremia during OI was suggested by a recent study demonstrating that lymphoid tissue macrophages produce high levels of HIV in the setting of OI (172).

Continuation of the role of immune stimulation in HIV replication was further substantiated in studies demonstrating that administration of HIV-infected subjects with influenza (173) or hepatitis B virus (174) antigens results in increased viral load and increases in plasma viremia. Furthermore, PSMC from HIV-infected subjects were rendered more susceptible to HIV infection *in vitro* following immunization with tetanus toxoid (175).

Long-term retroviral reservoirs: a model to study host factors in the pathogenesis of HIV disease

Development of a long-term retroviral reservoir is a critical step in HIV pathogenesis, and the mechanism of its formation is an important area of research. The reservoir is a source of persistent viral replication and is a major barrier to eradication of HIV infection (176).

trary, however, a reasonable consensus definition (including identification of HIV infection for more than 2 years, a CD4⁺ T cell count greater than 600 cells/mm³ without significant decline over time, an absence of HIV-induced disease, and no history of antiretroviral therapy) (184). Although a minority of cases of long-term non-progressing HIV infection may be associated with attenuated strains of HIV (185-188), most data suggest that viral attenuation is rare among long-term non-progressors, and that host factors play a dominant role in determining the state of non progression (183, 181, 190-192).

Genetic factors

Host genetic factors influence the rate of disease progression in HIV infection. A number of different mechanisms may be responsible for the observed associations between certain HLA haplotypes and different rates of HIV disease progression (193-196). The ability of certain HLA molecules to efficiently present immunodominant viral epitopes in order to generate cell-mediated immune responses may explain an association with slow disease progression. Conversely, other HLA molecules may promote immunopathogenic responses associated with more rapid disease progression. In a recent study, HLA-B*27, B*57, and B*51 were most strongly associated with slow progression of HIV disease, while HLA-A*23, B*37, and B*49 were associated with rapid progression (196). An HLA profile was developed that distinguished a 6-fold difference between rates of disease progression in rapid versus slow progressors. Other genetic factors linked to rates of HIV disease progression include allelic forms of the vitamin D-binding factor (197), variant alleles of mannose-binding lectin (198) and the TNF- α microsatellite allele (199).

CCR5 is a major co-receptor for M-tropic strains of HIV-1 (200-202). A mutant allele of the CCR5 gene that contains an internal 32 base pair deletion resulting in a truncated protein (200-202) has a major impact on susceptibility to HIV infection and on rates of disease progression in HIV-infected individuals. Homozygosity for the CCR5 mutation results in near-total protection from HIV-1 infection (200, 202-207). Heterozygosity for the CCR5 mutation results in decreased expression of CCR5 on the cell surface and reduced infectability of CD4⁺ cells with M-tropic strains of HIV-1 compared to CD4⁺ cells from CCR5 wild-type individuals (208). Although heterozygosity for CCR5 does not appear to afford protection against HIV-1 infection, it may confer partial protection against disease progression in HIV-infected individuals (194, 202-204, 209, 210). Protection against disease progression in CCR5 heterozygotes is due in part to the lower viral

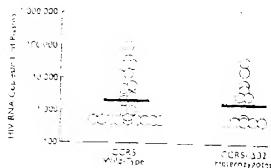


Fig. 3. Levels of plasma viremia are undistinguishable among HIV-infected long-term non-progressors stratified by CCR5 genotype. Dark bars represent median values.

load ("set point") after HIV seroconversion and a slower rate of CD4⁺ T-cell depletion compared with CCR5 wild-type individuals (204).

Heterozygosity for the CCR5 mutation is significantly more common in cohorts of HIV-infected long-term non-progressors compared to HIV-infected control populations (159, 201, 209, 210). However, despite the fact that the frequency of CCR5 heterozygotes is increased 2-fold among non-progressors compared to HIV-infected controls, and lower than 50% of non-progressors are CCR5 heterozygotes (201, 209). The possibility that CCR5 heterozygotes might constitute a subgroup among non-progressors with the lowest viral loads and most preserved CD4⁺ T cell counts was investigated. Interestingly, CCR5 wild-type and heterozygotes were not significantly different with respect to multiple immunologic and virologic parameters of disease activity (200). Mean CD4⁺ T cell counts were 973 cells/mm³ among CCR5 wild-type non-progressors and 885 cells/mm³ among CCR5 heterozygous non-progressors. Median levels of plasma viremia were 2,000 HIV RNA copies/mL among CCR5 wild-type non-progressors and 490 HIV RNA copies/mL among CCR5 heterozygous non-progressors (201, 211, 1).

We have previously demonstrated that, in contrast to individuals with progressive disease, HIV-positive long-term non-progressors maintain intact lymphoid tissue architecture (184, 212). However, a great deal of heterogeneity among non-progressors is evident in the degree of lymphoid hyperplasia and viral titers within germinal centers (184, 213). When stratified according to CCR5 genotype, wild-type and heterozygous non-progressors were equally likely to display a hyperplastic lymphoid architecture.

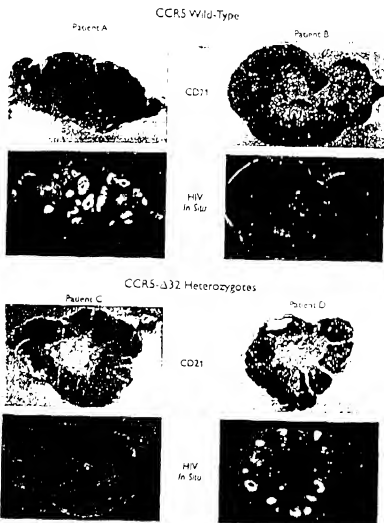


Fig. 1. The degree of follicular hyperplasia and the degree of virus trapping in lymph node germinal centers are indistinguishable among HIV-infected, long-term non-progressors stratified by CCR5 genotype. (A) HIV-infected, long-term non-progressor with CCR5 wild-type germinal center hyperplasia. (B) HIV-infected, long-term non-progressor with CCR5 $\Delta 32$ heterozygous germinal center hyperplasia. (C) HIV-infected, long-term non-progressor with CCR5 $\Delta 32$ heterozygous germinal center hyperplasia. (D) HIV-infected, long-term non-progressor with CCR5 $\Delta 32$ heterozygous germinal center hyperplasia. (A, B) CD21 staining. (C, D) HIV In Situ.

Taken together, these data indicate that although CCR5 heterozygotes have an increased chance of becoming non-progressors, HIV-infected CCR5 wild-type individuals may arrive at the same end point through one or more other mechanisms.

Host immune response CTL response

HIV-specific CTL play an important role in the control, albeit incomplete, of HIV replication and spread (212, 213). High precursor frequencies of HIV-specific CTL with broad specificity have been consistently linked to long-term non-progressors compared to progressors (180, 214–217). Quantitative aspects of the HIV-specific CTL response are also important determinants of the efficacy of the CTL response in controlling viral replication. Maintenance of CTL responses specific for

core coat proteins is associated with a decreased risk of disease progression (217, 218). This association does not appear to be true for CTL responses against other viral proteins. Recognition of a restricted number of CTL epitopes, particularly in particular MHC class I alleles may result in lower anti-HIV activity (219) and this in part explains the association of certain MHC class I alleles with slower progression to HIV disease (220–222). Furthermore, the skewing of the T cell response to HIV epitopes in HIV-infected patients has suggested differential recognition of HIV-specific CTL response components in a heterozygous group of individuals during primary infection associated with better clinical outcome (223). The ability of long-term non-progressors to maintain and produce high levels of CTL is not clear (224, 225). The maintenance of high levels of CTL is not clear in the context of the CCR5 $\Delta 32$ heterozygotes. This appears to be a strong hypothesis for future research in this area.

of lymphocyte maturation might allow that rapidly and completely modulate the host CTL response resulting in CTL exhaustion (i.e. high time tolerance) (22). CTL exhaustion may occur to some degree in HIV infection where disappearance of certain originally expanded CTL clones may can be demonstrated in the absence of viral escape mutations that might otherwise explain the phenomenon (22).

Taken together, these observations argue against an immunopathogenic role for CTL in HIV disease (23) and in favor of a salutary role in the maintenance of low viral load and the state of non progression. This inference is further supported by the demonstrated role of CTL in reducing levels of plasma viremia during primary HIV infection (24-26), and the association of progression to AIDS with viral escape from a long-lived (9-12 years) immunodominant CTL response (26).

The host CTL response against HIV is constrained by the ability of the host's MHC class I alleles to bind various viral peptides, while the virus is constrained by the degree to which an escape mutation impairs viral fitness. These host-virus dynamics are extraordinarily complex given the large number of permutations of viral epitopes and MHC class I alleles. Viral mutations within CTL recognition epitopes (i.e. "escape mutants") are associated with increased levels of viral replication and progression in HIV disease (22b-229). Viral escape mutants may thrive due to the release of CTL control over their replication and may also inhibit CTL responses against the pre-escape viral epitope (310-311). However, certain viral escape mutations may be costly to viral fitness. In this regard, it has been reported that diffuse infiltrative CD8 lymphocytosis in HIV infection was associated with certain HLA types that apparently constrain evolution of viral sequence diversity in the envelope V3 loop (332). Other studies have highlighted the constraints on the host CTL response imposed by MHC class I

genes. It has been reported that in an HIV-infected individual, CTL clones specific for an HLA-B*57-restricted epitope of gp120 displayed very limited diversity of T-cell receptor utilization (233). Furthermore, a marked diversity of certain CTL responses in individuals with viral load stability, where the dominant CTL response may initially be directed at the pre-escape viral epitope, has been demonstrated (21-233). The possibility that increased plasticity in the CTL response may allow the host to maintain more a stimulus and effective control over viral replication was suggested by studies demonstrating increased viral sequence diversity after generation of highly resistant escape mutants-specific CTL responses in slow progressors (236-237). Analyses of the role of CTL virus dynamics have been proposed that restriction of viral progression is a result of viral sequence variation that results in immunodominant CTL

response and shifts the host response towards a wicket epitope (238). Thus, disease progression may be the result of viral escape mutants overpowering the host CTL response, while slow progression may be the result of CTL plasticity overpowering viral escape mutants with limited fitness (238).

CD8+ T-cell phenotype

In viral studies, a more extensive role for CD8+ T cells may also play a role in non-progression of HIV infection. CD8+ T cells destroyed by Walker et al. (239-240) a non-cytolytic and non-MHC-restricted, which is viral replication at the level of HIV RNA transcription (241-243). This previously unknown cytotoxic CD8+ T cell activity was found to correlate with stage of disease (239). Lower CD8+ T cells from asymptomatic patients without significant CD8+ T cell alteration were required to suppress viral replication (244) compared to CD8+ T cells from patients with advanced stage HIV disease. Studies of long-term non-progressors have demonstrated more potent CD8+ T cell derived soluble antiviral responses compared with progressors (245-246).

CANTES MIP-1 α and MIP-1 β are also important antiviral chemokines secreted by CD8+ T cells as well as other cell types (247-249). These chemokines are natural ligands for the chemokine receptors CXCR4 and HIV co-receptor CCR5 and inhibit viral replication primarily at the cell-surface. Conflicting data have been obtained regarding a relationship between levels of these chemokines and progression of HIV disease (251-249-253). These conflicting data are not surprising since they come from studies where exogenous PBMC or T-cell supernatants, however, suggesting a possible role for the CD8+ T cells in the protection of some exposed uninfected individuals against HIV infection. Upon stimulation with HIV antigen, CD8+ T cells from these individuals secreted high levels of these chemokines that were capable of blocking the replication of HIV and strains of HIV in cell lines. Primary levels of expression of these chemokines were not directly related to the degree of HIV replication in cell lines (254). This is relevant information with regard to the role of these chemokines in progression.

CD8+ T-cell derived chemokines have been shown to inhibit HIV infection in T cells which are infected by HIV. The chemokine MIP-1 α is a natural ligand for CXCR4, which has been shown to be important for HIV infection. CD8+ T cells from slow progressors were able to inhibit HIV infection in T cells (255). CD8+ T cells from fast progressors were unable to inhibit HIV infection in T cells (256). This suggests that the ability of CD8+ T cells to inhibit HIV infection may be related to the degree of viral progression. This is consistent with the idea that the ability of CD8+ T cells to inhibit HIV infection may be related to the degree of viral progression.

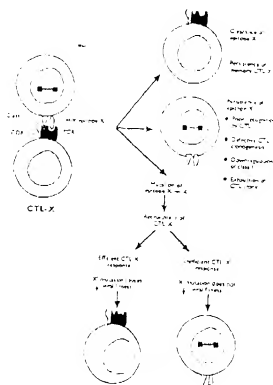


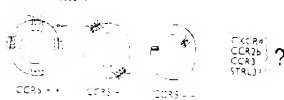
Fig. 3. The possible outcomes following CTL recognition of an HIV epitope are complex. An efficient CTL response against epitope X may result in clearance of the epitope and persistence of memory CTL (top right). Persistence of the viral epitope may be the result of a variety of factors, including poor recognition of the epitope by CTL, ineffective downregulation of the CTL, downregulation of MHC class I molecules by viral proteins, and/or exhaustion of the CTL clone (middle right). Alternatively, a CTL escape mutation may occur in the epitope (bottom right). The outcome in this situation depends both on the relative efficiency of the CTL response directed against the escape mutant as well as on the relative cost of the mutation to viral fitness.

receptors may occur by virtue of genetic polymorphisms (i.e. CCR5-Δ32) or by downregulation of their messenger RNA by host protein products (748). Alternatively, upregulation of the natural ligands of the HIV co-receptors may prevent HIV access to functional co-receptors and thereby limit infection of target cells. However, it is important to appreciate other circumstances of acceptance of HIV co-receptors by their natural ligands. As noted above, high concentrations of RANTES, MIP-1 α , and MIP-1 β may inhibit entry and replication of HIV strains in HIV, however, they may also represent a selective pressure by the host immune system that may favor the emergence of HIV strains that are resistant to CCR5 and CXCR4. A similar argument may be made that may actually enhance resistance to HIV strains that are resistant to CCR5 and CXCR4.

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Genetic Factors



Immunoregulatory Factors

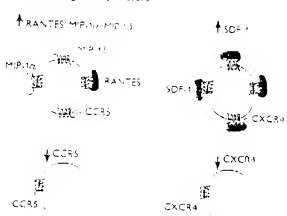


Fig. 5. Genetic as well as immunoregulatory factors govern the availability of functional HIV co-receptors. The CCR5-Δ32 allele encodes a molecular that does not function as an HIV coreceptor. Individuals who are homozygous for this mutant allele are afforded resistance to HIV infection, whereas heterozygotes are partially protected against disease progression. Polymorphisms in other co-receptor genes (i.e. CXCR4) also correlate with early or disease progression. The upregulation of the co-receptor ligands (i.e. RANTES, MIP-1 α , and MIP-1 β) and SDF-1 in the context of HIV infection and/or downregulation of co-receptors (i.e. CCR5 and CXCR4) may also govern the availability of functional co-receptors.

data). These possibilities were not satisfactory not only because the strategies that employed these factors for their induction (144). Finally, the induction of these factors by a selective antigenic factor (145) may be a more effective strategy for the induction of these factors and thereby enhance the resistance to HIV infection (146).

Therapeutic Approaches

The combination therapy of zidovudine, zalcitabine, and didanosine, plus zalcitabine, plus didanosine (150). Nonnucleoside reverse transcriptase inhibitors (NNRTIs) such as zalcitabine, didanosine, and zalcitabine (151) have been shown to be effective in the treatment of HIV infection. The combination of these drugs with zalcitabine and didanosine may be a more effective strategy for the treatment of HIV infection.

- [illegible]

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